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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER

DUFFY, PATRICIA ANN

ART UNIT	PAPER NUMBER
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1645

DATE MAILED: 08/29/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/063,692

Applicant(s)

EATON ET AL.

Examiner

Patricia A. Duffy

Art Unit

1645

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-20 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 1-20 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 08 May 2002 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. ____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 2002.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. ____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: sequence attachments.

DETAILED ACTION

The preliminary amendments filed 9-10-02 has been entered into the record.
Claims 1-20 are pending.

Priority

Applicant's claim for domestic priority under 35 U.S.C. 119(e) is acknowledged. However, the provisional application upon which priority is claimed fails to provide adequate support under 35 U.S.C. 112 for claims 1-20 of this application.

According to the priority statement of 9/10/02, it appears that the claimed subject matter defined in the instant application is not supported by the parent application serial no. 10/006,867. Based on the information given by applicant and an inspection of the patent applications, the examiner has concluded that the subject matter defined in this application is not supported by the disclosure in any of the applications for which Applicants claim priority because the claimed subject matter does not have utility, enablement or written description in any of the prior applications for reasons set forth herein. Accordingly, the subject matter defined in claims 1-20 has an effective filing date of 5-8-02.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 5-8-02 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 5-8-02.

Drawings

The drawings in this application have been approved by the Draftsperson. No further action is required by Applicants.

Specification

The disclosure is objected to because of the following informalities:

The lengthy specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors of which applicant may become aware in the specification.

The title and abstract of the invention are not descriptive of the now claimed invention. A new title and abstract are required that is clearly indicative of the invention to which the claims are directed.

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code at least at page 35. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. Applicants should review the lengthy specification for other browser-executable code and delete or amend appropriately.

The use of the trademark ATCCTM has been noted in this application. They should be capitalized wherever it appears and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks. For example, the trademark American Type Culture Collection (ATCCTM) needs to be recognized wherever it appears.

Information Disclosure Statement

The information disclosure statement filed 9-17-02 has been considered with the exception of the BLAST sequences. The BLAST results demonstrate that applicants are aware of nucleic acids with identity/homology to the one claimed herein. However, as the BLAST results do not give sufficient identifying information, the Examiner cannot determine if said sequences constitute prior art.

An initialed copy is enclosed.

Claim Objections

Claims 1-20 are objected to because of the following informalities: the claims improperly reference Figures. Referencing figures in a claim is only proper when the information contained therein cannot be represented in any other manner (MPEP 2173.05(s)). Further, the sequence rules require sequences to be claimed by their appropriate sequence identifier number and not Figure number. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title.

The pending claims have been reviewed in light of the Utility Examination Guidelines and Guidelines for Examination of Patent Applications under 35 USC 112, first paragraph, "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1092-111, Friday, January 5, 2001.

Claims 1-20 are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility due to its not being supported by a specific, substantial and credible utility or, in the alternative a well-established utility.

The claims are drawn to a nucleic acid encoding the polypeptide shown in Figure 38 (SEQ ID NO:38), fragments and percentage variants thereof encoded by SEQ ID NO:38. The nucleic acid of SEQ ID NO:37 corresponds to PRO1344 a cDNA corresponding to DNA 58723-1588 referenced in the specification. The specification does not disclose any secondary or tertiary structural features of this polypeptide, nor does it assert that the polypeptide has any homology with known, characterized polypeptides. The instant specification does not disclose any additional information regarding PRO1344 such as subcellular location, timing of regulation during cellular differentiation, which hormones or transcription factors regulate PRO1344, and what physiological significance PRO1344 plays. Therefore, it is a totally new, uncharacterized polynucleotide and polypeptide with no well-established utility.

The specification generally asserts that all of the disclosed PRO polynucleotides will be useful for a number of purposes; however, none of these asserted uses meet the three-pronged requirement of 35 U.S.C. § 101 regarding utility, namely, that the asserted utility be credible, specific and substantial. The asserted utilities will each be addressed in turn.

1) the PRO polynucleotide can be used as hybridization probes to isolate similar sequences, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, and in the recombinant production of the encoded polypeptide: This asserted utility is not specific or substantial. Since the same can be done with any polynucleotide, the asserted utility is not specific to the claimed PRO1344 polynucleotides. Furthermore, since the specification does not disclose how PRO1344 can be used, significant further research would be required of the skilled artisan to determine how to use the

polynucleotide or the encoded polypeptide. Since the asserted utility is not presented in a ready to use, real-world application, the asserted utility is not substantial.

2) the PRO polynucleotide can be used to make knock-in or knock-out transgenic animals: This asserted utility is not specific or substantial. Since the same can be done with any polynucleotide, the asserted utility is not specific. Also, the specification does not provide any information regarding the phenotype of the resulting animals, or what they can be used for (e.g., a model system for a specific disease). Therefore, the asserted utility is not substantial, as further research would need to be done before the asserted utility is in currently available form.

3) the PRO polynucleotide can be used in gene therapy: This asserted utility is not specific or substantial. Since a defect in any polypeptide is likely to cause a disease of some sort, every polynucleotide encoding a polypeptide is a target for gene therapy. Thus, the asserted utility is not specific to the claimed PRO1344 polynucleotide. Furthermore, the specification does not disclose a nexus between any specific disease states and a change in amount or form of PRO1344. Significant further research would have to be conducted to identify such a nexus. Therefore, the asserted utility is not substantial.

4) the PRO polynucleotide can be used in tissue typing: This asserted utility is not specific or substantial. With the exception of a few housekeeping genes, all polynucleotides have a tissue specific pattern of expression, and thus virtually any polynucleotide can be used in tissue typing. Thus, the asserted utility is not specific to PRO1344.

5) the PRO polynucleotide can be used to screen for compounds that interact with it: Since the same can be done with any polynucleotide, the asserted utility is not specific to the claimed PRO1344 polynucleotides. Furthermore, since no activity has been assigned to PRO1344, the compounds identified by such screening would have to be subjected to rigorous experimentation to determine how they are useful. Therefore, the asserted utility is also not substantial.

6) the Pro polynucleotide can be used in tumor/cancer diagnostics or therapeutics:

The specification also discloses that PRO1344 was tested using quantitative PCR amplification reactions with cDNA libraries isolated from different human tumor and normal human tissue samples and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the nucleic acid encoding the PRO polypeptide (specification page 140). The specification teaches that the differential expression in one or more tumor tissues as compared to one or more normal tissues of the same tissue type renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor as well as therapeutically as a target for the treatment of a tumor in a subject possession such a tumor. mRNA encoding the PRO1344 polypeptide (DNA58723-1588) was reported as "more highly expressed in" normal stomach, kidney tumor and normal skin as compared to a stomach tumor, normal kidney and melanoma tumor (specification page 141). The specification is devoid of teaching of the number of samples tested, the statistical significance if any of the "more highly expressed" and the specific probe used for the alleged quantitative analysis performed. The data presented are not quantitative and as such, the relevance as compared to the recited control is ambiguous. Further, it appears that normal cells such as stomach and skin express the nucleic acid more highly as compared to tumors. As such, since the cDNA, proteins or antibodies are not described as being specifically correlated with a specific type of cancer the skilled artisan could not distinguish tumors from non-tumors based on the alleged "more highly expressed" criteria only. Therefore, the asserted use as diagnostic marker or targets of therapeutic intervention are not persuasive to impart a specific utility. This relevance of the asserted higher expression very vague, and does not disclose what mathematical calculations, if any, were used to establish significance of the finding across a variety of samples from different patients. Therefore, the apparent single data point presented in the quantitative PCR is preliminary at best, and cannot be evaluated or repeated independently

by the skilled artisan. Clearly, further research would be required of the skilled artisan to establish the statistical significance if any, and whether and how a probe used in the PCR assay could be used as diagnostic markers or therapeutic targets. Such further experimentation indicates that the asserted utility is not in currently available form for the disclosed nucleic acid of SEQ ID NO:37. Furthermore, the literature indicates that such results are to be evaluated very critically. For example, Hu et al. (2003, Journal of Proteome Research 2:405-412) analyzed 2286 genes that showed a greater than 1-fold difference in mean expression level between breast cancer samples and normal samples in a microarray (p. 408, middle of right column). Hu et al. discovered that, for genes displaying a 5-fold change or less in tumors compared to normal, there was no evidence of a correlation between altered gene expression and a known role in the disease. However, among genes with a 10-fold or more change in expression level, there was a strong and significant correlation between expression level and a published role in the disease (see discussion section). Therefore, in the absence of a statistical significance of the data and quantitative evaluation it would appear that the relationship between the reported "higher expression" as it relates to tumor formation and role in tumor formation or role in normal cells remains to be established. Consequently, any relevance with respect to using the nucleic acid, protein or antibody for therapeutic purposes remains to be established. With respect to the nucleic acids encoding the polypeptides, it is noted that the art establishes that increased mRNA production does not necessarily lead to increased protein production. Haynes et al. (Electrophoresis, 19:1862-1871, 1998) found "a general trend" but no significant correlation between nucleic acid level and translation and protein levels. Further, Haynes et al teach that polypeptide levels cannot be accurately predicted from mRNA levels and that variances as much as 40-fold or even 50-fold were not uncommon (p 1863). Haynes et al used yeast as an art-accepted model for eukaryotic systems. Further, the lack of demonstrable correlation of mRNA expression levels with protein levels was so well known in the art at the time of filing, it was reported in a general text

book. Lewin (*Genes VI* (1997) Chapter 29, pages 847-848) teaches that the concept that transcription levels do not correlate with protein levels was so well known to the art that it was presented in a textbook. Lewin, *Genes VI* (1997) Chapter 29, pages 847-848 which specifically teaches "... production of RNA cannot be inevitably be equated with production of protein...." (page 487, column 2, last paragraph). This concept reconfirmed by a variety of studies such as that evidenced by Gokman-Polar et al (*Cancer Research* 61:1375-1381, 2001) that indicates the absence of any necessary correlation between increased mRNA levels and increased protein levels. Gokman-Polar et al that teach "Quantitative reverse transcription-PCR analysis revealed that the PKC mRNA levels do not directly correlate with PKC protein levels, indicating that PKC isoenzyme expression is likely regulated at the posttranscriptional/translational level" (see abstract). Gokman-Polar et al show in Figure 6-7 that there is no increasing mRNA expression for any of the isoenzymes, while the protein is significantly overexpressed as shown by Figure 4-5. Anderson et al teach that "Despite extensive work on the regulation of many individual genes, little attention appears to have been paid to the global question of the relation between mRNA and corresponding cellular protein abundances.." (Anderson et al, *Electrophoresis*, 18:533-537, 1997; see page 536, column 2.). Anderson et al teach that the correlation is 0.48 and indicates that the two major phases of gene expression regulation are of approximately equal importance in determining the net output of protein. Reanalysis of the data of Kawamoto et al, indicates that the correlation coefficient is poor when one gene product, well separated from the gene cluster is omitted from the calculation (Anderson et al page 536, column 2, first full paragraph). Further, the lack of correlation between mRNA levels and protein levels in cancer is demonstrated by Chen et al (*Molecular and Cellular Proteomics*, 1:304-313, April 2002). Chen et al indicate that "Using a quantitative analysis of mRNA and protein expression within the same lung adenocarcinomas, we showed that only a subset of the proteins exhibited a significant correlation with mRNA abundance." (see Chen et al page 304, column 1, abstract). As such, not all cancer protein have a correlation and

therefore, in the absence of any specific evidence to the contrary with respect to the polypeptide, variants thereof or antibodies that bind them, there is reason to doubt the asserted truth of the assertion of utility. Therefore, the skilled artisan immediately recognizes that, at the time of the invention, that no direct correlation between gene amplification/mRNA levels and increased polypeptide levels necessarily exists, no dogma exists between mRNA and polypeptide levels (for which neither are disclosed within the instant specification for polypeptide). Given the totality of the evidence provided by Haynes et al, Anderson et al, Chen et al and Lewin et al, it is clear that those skilled in the art would not assume that an alleged increase in gene copy number or increase in mRNA levels would correlate with increased polypeptide levels. One skilled in the art would have to do further research to determine whether or not the polypeptide levels were higher, and whether the higher levels were statistically significant. As such, the claimed nucleic acid encoding the protein does not have utility, because the protein *per se* has no utility.

Thus, the proposed use of the PRO1344 polynucleotides as diagnostic markers and therapeutic targets are simply starting points for further research and investigation into potential practical uses of the polynucleotides, encoded polypeptides and antibodies that bind the polypeptides. "The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility", [u]nless and until a process is refined and developed to this point-where specific benefit exists in currently available form- there is insufficient justification for permitting an application to engross what may prove to be a broad field", and "a patent is not a hunting license". "[i]t is not a reward for the search, but compensation for its successful conclusion." Similarly, the other listed and asserted utilities in the specification as exemplified by the other Examples are not particularly disclosed with respect to the claimed polynucleotide encoding a protein or are neither substantial nor specific due to being generic in nature and applicable to a myriad of such proteins. (*Brenner v. Manson*, 148 USPQ 689 (Sus. Ct. 1996). Additionally, the courts have

held that the disclosure is insufficient when testing is necessary to determine the actual use or possible lack of use (In re Kirk and Petrow (CCPA) 153 USPQ 48). Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed. Neither the specification as filed nor any art of record discloses or suggests any property or activity for the nucleic acid per se, the polynucleic acid encoding the PRO polypeptide or the anti-PRO antibody that binds the polypeptide such that another non-asserted utility would be well established for the instantly claimed compounds.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-20 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claims 1-6, 9, 10 and 14-20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

The claims are drawn to nucleic acids encoding polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity with a particular disclosed sequence or a sequence that hybridizes to a particular sequence. The claims are also drawn to fragments such as "the extracellular domain of a polypeptide lacking its associated signal peptide" or "the extracellular domain" of the polypeptide *per se*. The claims do not require that the nucleic acid possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity or undefined structure.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity or undefined fragment thereof. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written

description' inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polynucleotides and encoded polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Further, the specification and Figure 38 in particular, does not teach the claimed extracellular domain structure of SEQ ID NO:38. The specification does not teach any subsequence of the polypeptide of SEQ ID NO:38 or Figure 38 that corresponds to an extracellular domain or extracellular domain lacking a signal sequence as recited in the claims. Therefore, the specification as filed does not set forth in a clear manner or in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the variants or fragments of the polypeptide as now claimed.

Therefore, only an isolated nucleic acid encoding a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:38, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claims 1-6 and 13-20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The specification at pages 120-123 lacks complete deposit information for the deposit of the full length cDNA encoding the claimed polypeptide deposited at the American Type Culture Collection as set forth in embodiment (e) of claims 1-6, 13, 14 and claims 15-20 as dependent there from. It is not clear that the deposit is known and publicly available or can be reproducibly isolated from nature without undue experimentation or if it is the same as SEQ ID NO:37 encoding the polypeptide of SEQ ID NO:38 or contains additional nucleic acid sequences that encode additional amino acid residues. As such, a deposit for patent purposes is required. The referral to the deposit on page 123 is an insufficient assurance that all required deposits have been made and all the conditions of 37 CFR 1.801-1.809 have been met. The specification states that pursuant to an "agreement" between Genentech, Inc. and the ATCCTM, permanent unrestricted availability to the public of the progeny of the culture upon issuance of "the pertinent US Patent" is provided for. This is insufficient because agreements are contracts that are revocable and the conditions therein are revocable. Further, it is unclear what would be considered the "pertinent US Patent". As such, Applicants are required to provide assurances that All restrictions upon public access to the ATCCTM accession number 203133 as specifically claimed, will be "irrevocably removed upon the grant of a patent from this application" specifically using this exact language. Since "agreements" are subject to revocation, this assurance is required for patent purposes. The assurances should be made by an affidavit or declaration by Applicants or Assignees or a statement by an attorney of record who has authority and control over conditions of the deposit over his or her signature and registration number. Applicants are specifically

directed to MPEP 2424.01 that states "with one possible exception (37 CFR 1.808(b)), that all restrictions on the accessibility be irrevocably removed by the applicant upon the granting of the patent" are required see *Ex parte Hildebrand*, 15 USPQ2d 1662 (Bd. Pat. App. & Int. 1990). Further, the statement is not in compliance with MPEP 1.806 that requires "A deposit made before or during pendency of an application for patent shall be made for a term of at least thirty (30) years and at least five (5) years after the most recent request for the furnishing of a sample of the deposit was received by the depository. In any case, samples must be stored under agreements that would make them available beyond the enforceable life of the patent for which the deposit was made."

Claims 1-6, 9, 10, 14-20 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

As to all of the recited claims. The claims comprise the limitations that the claimed nucleic acid encoding the polypeptide comprise an "extracellular domain" or "the extracellular domain lacking its associated signal peptide", and "the extracellular domain" is not defined in the specification or claims. These limitations are indefinite because neither the figure nor the specification define or teach the metes and bounds of these specific fragments. Further, if the protein has an extracellular domain, the recitation of "the extracellular domain"... "lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of protein production in the cell.

Additionally, claim 15 recites "hybridization under stringent conditions". Neither the specification nor the art define these conditions unambiguously. Therefore, the skilled artisan would be unable to determine the metes and bounds of the claimed invention in the absence of a recitation of clear, definite hybridization conditions in the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 1-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Baker et al (WO 99/63088, published 12-9-99).

Baker et al teach a nucleic acid that is 100% identical as compared to SEQ ID NO:37 and encodes a polypeptide of SEQ ID NO:38 (see attached alignment). Baker et al teach the mature protein lacking the signal sequence (see pages 147-149). Baker et al teach the nucleic acid in an expression vector and the expression vector in a suitable host cell such as E. coli, yeast or CHO cells (see pages 352-355). As such Baker et al anticipates the instantly claimed invention.

Claims 1-6, 9, 10 and 14-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Barnes et al (WO 00/18904, published 06 April 2000).

Barnes et al teach a nucleic acid encoding a protein named Tango 215. The nucleic acid of Barnes et al is 99% identical as compared with SEQ ID NO:37 and encodes a polypeptide that is 99.8% identical as compared with SEQ ID NO:38 (see attached alignments). Barnes et al teach the mature polypeptide (i.e. lacking the signal sequence at page 46). Barnes et al teach expression vectors and host cells comprising the expression vectors. Barnes et al teach *E. coli*, yeast cells and mammalian cells as host cells for recombinant production of the encoded protein (see page 5, lines 10-19; page 76-83). Barnes et al teach nucleic acids that hybridize to the nucleic acids described therein under standard conditions and fragments thereof (see page 49, lines 14-29 and page 53). In the absence of a defined extracellular domain in the specification and the claims, the nucleic acid of the prior art is deemed 100% identical to an extracellular portion of the claimed nucleic acid and as such meets the Markush members (c-d) of claims 1-6, 14-16 and dependent claims 9, 10 and 17-20. Further, the prior art meets claims 1-5 as it anticipates embodiments (a, b, e, f and g).

Claims 14-16 are rejected under 35 U.S.C. 102(e) as being clearly anticipated by Robinson et al (US Patent No. 6,331,427 issued 12-18-01, filed March 26, 1999).

Robinson et al teach SEQ ID NO:179. SEQ ID NO:179 is 99.8% similar to residues 381-800 of SEQ ID NO:37 (see attached alignment). The sequences have more than 100 consecutive nucleotide residues that are identical. Therefore, the sequence of the prior art would inherently hybridize to SEQ ID NO:37 or any of the nucleic acids encoding SEQ ID NO:38.

Since the Office does not have the facilities for examining and comparing applicant's nucleic acid with that of the prior art, the burden is on applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the nucleic acid of the prior art does not possess the same functional

characteristics of the claimed nucleic acid). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 619 F.2d 67, 205 USPQ 594 (CCPA 1980).

Status of the Claims

Claims 1-20 stand rejected.

Conclusion

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Patricia A. Duffy whose telephone number is 571-272-0855. The examiner can normally be reached on M-Th 6:30 am - 6:00 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith can be reached on 571-272-0864.

The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Pat. A. Duffy
Patricia A. Duffy, Ph.D.
Primary Examiner
Art Unit 1645

Duffy, Patricia

From: Duffy, Patricia
Sent: Monday, August 16, 2004 6:22 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/063692

Importance: High

In re:10/063,692

Please search SEQ ID NOs:38 and 37 and oligomers thereof.
Please run the amino acid sequence of SEQ ID NO:38 against the NA database.
Please perform a commercial and interference database search.

Please print out top 100 hits in each of the above.

Thank you.

Patricia A. Duffy, Ph.D.
Art Unit 1645, Remsen 3B05
571-272-0855

Wx notes

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMDGYQHLHTQLQYECISPFYRRLGSSRRRTCLRTGKWSGRAPSCIPICGIENITAP
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAACHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRS PGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

no extracellular domain

EXPLANATIONS

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTGCTGGACGAGTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCTTGGCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGAGTGTGTG
AATATGATCAGATTGAGTGGCTGCCCCGGAAGAGGGAAGTCGTGGGTATACCATCCCTTGTGTCAGGAATGAGGAGAA
TGAGTGTGACTCCGCTGATCCACCCAGGTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGGTCTACTGTGCAGAGTGGCAGCAGGCTGGTACGGAGGAGACTGTCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGC
TAAACCTGGGTTTGTCACTCACTAAGATTGTGCTGTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGCTTCCATGCCATTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTTTCCATGACGGCAGCTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATATCGGGCAGCGCTGTGAAAATCTCCTTGAAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAAGAAA
TAACAGGGGGGCCGGGCTTATCAACGGACGCCATGCTAAATTTGGCAGCGTGGTGTCTTCTTTTGTAACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAGCTGCGCA
GAACCAAGATTTCAGACCTGGTGAGAGGAGAGTTCTTCGATGCAAGTTCACTCAAGGAGACACCAATTACACAGCTAT
ACTCAGCGGCTTCAGCAGCAGAACTGCAGAGTGGCCCTACCAAGAGCCAGCCCTTCCCTTTGAGATCTGCCCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTACCCCTTCTACCGCGCTGGGCGAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGCGGGGCACCATCTGCATCCCTATCTGCGGGAATTTGAGAACATCACTGCTCCAAAGA
CCCAAGGGTTGGCTGGCGTGGCAAGCAGCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCTACACAAGGGAGC
GTGGTTCTTAGTCTGCAGCGTGGCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAG
GTCCCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCTTGCATCCCACTATGACCCCATCTGCTTGTGCTGACATCGCCATCTTGAAGCT
CCTAGACAAGGCCCGTATCAGCAGCCGAGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCCCTCCAGAG
TCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGAGCTGAGGAGCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGCTGTGACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAAGTGGCT
GTGCCAGGCTTCTGACTTCAGGGACAAACTCAGTGAAGGGTGAAGTACCTCCATTGCTGGTAGGCTGATGCCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAGTAAGTTCTTCAAGAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCCTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCGTGGGACAGCCAGGGCAGCAGAGCTGGCATGTGGTGCATGCCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAATAAGGGTTGGCTTCT
GAACTACAAAAA
AAAAA

> 0 <
0|0|0 IntellGenetics
> 0 <

FASTDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-692-37.res made by tport on Thu Jul 105 11:38:51-PST.

Query sequence being compared: US-10-063-692-37 (1-2846)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-10-063-692-37 (1-2846) with:
File : aa339951.seq
File : aa265034.seq
File : abk30334.seq

```

100-
N -
U - 50-
M -
B -
E -
R -
O -
F - 10-
S -
E - 5-
Q -
U -
E -
N -
C -
S -
E -
SCORE 0 316 632 949 1265 1581 1897 2214 2530 2846
STDV -1 -1

```

PARAMETERS

Similarity matrix Unitary 1 K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 2189 Median 993 Standard Deviation 1038.28
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 8479
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Init. Opt.

Sequence Name Description Length Score Score Sig. Frame
1. aa265034 Membrane-bound protein PRO134 2846 2846 2846 0.63 0
The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
2. aa339951	Human TANGO 215 cDNA.	2747	2729	2729	0.52	0
3. abk30334	Human G-protein-coupled prote	2886	992	2506	-1.15	0

1. US-10-063-692-37 (1-2846)
aa265034 Membrane-bound protein PRO134 encoding cDNA.

Initial Score = 2846 Optimized Score = 2846 Significance = 0.63
Residue Identity = 100% Matches = 2846 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X 10 20 30 40 50 60 70
CGCTCGGCGACCAAGCGCGAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
CGCTCGGCGACCAAGCGCGAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
X 10 20 30 40 50 60 70

```

```

80 90 100 110 120 130 140
CCTTCTCATCTGCTCTGCGCAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
CCTTCTCATCTGCTCTGCGCAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
80 90 100 110 120 130 140

```

```

150 160 170 180 190 200 210
CATGTGTGGAGAGCTGTGTGATATGATCAGATTTGAGTGGCTGTGCTGCGGAGAGAGAGAGTGTGGGTTA
CATGTGTGGAGAGCTGTGTGATATGATCAGATTTGAGTGGCTGTGCTGCGGAGAGAGAGAGTGTGGGTTA
150 160 170 180 190 200 210

```

```

220 230 240 250 260 270 280
TACCAATCCCTTCTGCGCAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
TACCAATCCCTTCTGCGCAGAGATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
220 230 240 250 260 270 280

```

```

290 300 310 320 330 340 350
TGAATACTGCAAGAGCTGCGCAATATGCTCATGCGGCGGAGTACCTTGTGATGCAAGAGGTTCTA
TGAATACTGCAAGAGCTGCGCAATATGCTCATGCGGCGGAGTACCTTGTGATGCAAGAGGTTCTA
290 300 310 320 330 340 350

```

```

370 380 390 400 410 420 430
CTGTGCAAGAGTCCGAGAGAGCTGTGTGATATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
CTGTGCAAGAGTCCGAGAGAGCTGTGTGATATGAGCTGGGTGCTGAGACGACGAGGCGGCTCACTTTCTTCAGCT
370 380 390 400 410 420 430

```

```

440 450 460 470 480 490 500
GGGTGCAATTTTGTGGAAGCTTATCCCTTAATGCTCACTGTGATGCAAGAGGTTCTGAGAGGTTCTA
GGGTGCAATTTTGTGGAAGCTTATCCCTTAATGCTCACTGTGATGCAAGAGGTTCTGAGAGGTTCTA
440 450 460 470 480 490 500

```

```

510 520 530 540 550 560 570
TGTATCCCACTAAGATTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT
TGTATCCCACTAAGATTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT
510 520 530 540 550 560 570

```

```

580 590 600 610 620 630 640
TGTGATGAGAGACACCGCGATGCGCAGATCATACAGCTGTCTGTGCGACAGAGCGGCGGCTCTTATCCA
TGTGATGAGAGACACCGCGATGCGCAGATCATACAGCTGTCTGTGCGACAGAGCGGCGGCTCTTATCCA
580 590 600 610 620 630 640

```

[illegible][illegible]

[illegible]

[illegible][illegible]

3. US-10-063-692-37 (1-2846).
abk30334 Human G-protein-coupled protease #104.

Initial Score	=	992	Optimized Score	=	2506	Significance	=	-1.15
Residue Identity	=	97%	Matches	=	2699	Mismatches	=	33
Conservative Substitutions	=	45					=	0

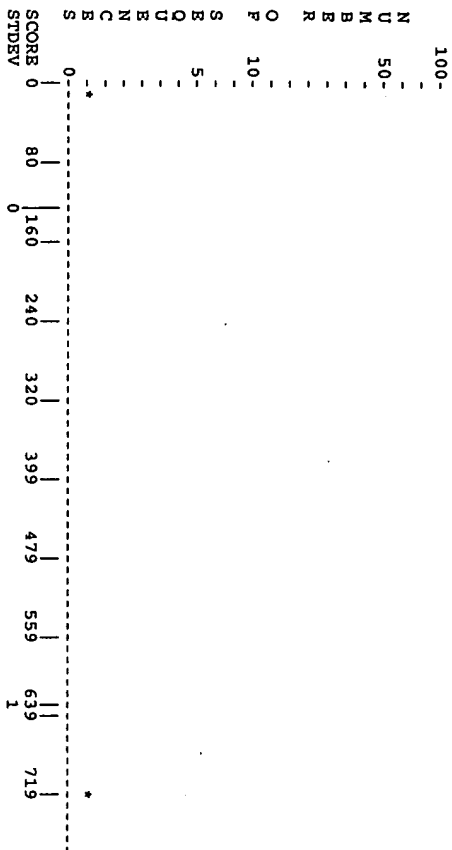
l
> 0 <
0 | 10
> 0 < Intelligenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-692-38.res made by tport on Thu Jul 105 11:41:34-EST.

Query sequence being compared: US-10-063-692-38 (1-720)
Number of sequences searched: 2
Number of scores above cutoff: 2

Results of the initial comparison of US-10-063-692-38 (1-720) with:
File : aaa39951.pep
File : aay88280.pep



PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 164
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 500
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 368 Median 19 Standard Deviation 495.68
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 962
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Int. Opt. Score	Sig. Frame
1. aay88280	Human TANGO 215 protein.	720	719	0.71 0
2. aaa39951	TOIG of: aaa39951 check: 738	242	18	107 -0.71 0

1. US-10-063-692-38 (1-720)
aay88280 Human TANGO 215 protein.

Initial Score = 719 Optimized Score = 719 Significance = 0.71
Residue Identity = 99% Matches = 718 Mismatches = 1
Gaps = 0 Conservative Substitutions = 1

X 10 20 30 40 50 60 70
MELGCMWQGLTFLQALLISLPREYVINEACGAEINIMCECCCEYDIECVCPKREYVYTIICCRNE
MELGCMWQGLTFLQALLISLPREYVINEACGAEINIMCECCCEYDIECVCPKREYVYTIICCRNE
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
ENECDSCLIHFGCTIFENCKSCRNCSGWTGTLDDFYVKGFFYCAECGAGMYGDCMRCCQVLAAPKQGLILBSY
ENECDSCLIHFGCTIFENCKSCRNCSGWTGTLDDFYVKGFFYCAECGAGMYGDCMRCCQVLAAPKQGLILBSY
X 80 90 100 110 120 130 140

150 160 170 180 190 200 210
PLNACGEMTHAKRGFVITQARFVMTSLFEDYMCQYDVEYVRDGNRGOIIRKCGNERPAPLOSISLHV
PLNACGEMTHAKRGFVITQARFVMTSLFEDYMCQYDVEYVRDGNRGOIIRKCGNERPAPLOSISLHV
X 150 160 170 180 190 200 210

220 230 240 250 260 270 280
LFHSDGSKNPFGRFAIYEIITACSSSPCFHDTGTCVLDKAGSYKACLAGYTGRCENILBERNCSDBGPVN
LFHSDGSKNPFGRFAIYEIITACSSSPCFHDTGTCVLDKAGSYKACLAGYTGRCENILBERNCSDBGPVN
X 220 230 240 250 260 270 280

290 300 310 320 330 340 350 360
GYOKITGPGELINGRAHAKIGTVVSPFCNNSYVLSGNEKRTCCQNGEMSGOPICIKACRPKISDLVRRVL
GYOKITGPGELINGRAHAKIGTVVSPFCNNSYVLSGNEKRTCCQNGEMSGOPICIKACRPKISDLVRRVL
X 290 300 310 320 330 340 350 360

370 380 390 400 410 420 430
PMQVQSRERPLHQLYSAAFSKQKQLQSAFPTKPPALPFDDLPNGYQHLHTQLQYECISPFYRLSSRRRTCLRT
PMQVQSRERPLHQLYSAAFSKQKQLQSAFPTKPPALPFDDLPNGYQHLHTQLQYECISPFYRLSSRRRTCLRT
X 370 380 390 400 410 420 430

440 450 460 470 480 490 500
GKMSGRAIPSCIPICGKIENITAPKTQGLRWPWQAALYRRTSGVHDSGLHKGAMFLVCSGLVNERTVVAH
GKMSGRAIPSCIPICGKIENITAPKTQGLRWPWQAALYRRTSGVHDSGLHKGAMFLVCSGLVNERTVVAH
X 440 450 460 470 480 490 500

510 520 530 540 550 560 570
CVTDLGKVTMIKTADLKVVLGKFFYRDDDDDEKTIQSLQISAILLHPYDILLDADIAIILKLDKARISTRV
CVTDLGKVTMIKTADLKVVLGKFFYRDDDDDEKTIQSLQISAILLHPYDILLDADIAIILKLDKARISTRV
X 510 520 530 540 550 560 570

580 590 600 610 620 630 640
OPICLAASRDLSSTFQESHITVAGMNVLDVRSPPGRNDTLRSGVSVVDSLLCEQHEHDHGIIPVSYTDNMF
OPICLAASRDLSSTFQESHITVAGMNVLDVRSPPGRNDTLRSGVSVVDSLLCEQHEHDHGIIPVSYTDNMF
X 580 590 600 610 620 630 640

650 660 670 680 690 700 710
CASWEPYAPSDICTTAETGGIAAVSPFGARSPBPRWHLKMGVSVSYKTSRSLSTAFKVLPRKNIERNMK
CASWEPYAPSDICTTAETGGIAAVSPFGARSPBPRWHLKMGVSVSYKTSRSLSTAFKVLPRKNIERNMK
X 650 660 670 680 690 700 710

CASNEPTAPSDICTAETGIAVSPFGRASBPFRMHLMGLVMSYDXTCSHRUASTAFTKVLPEFKWIERNMK
650 660 670 680 690 700 710 720

2. US-10-063-692-38 (1-720)

aaa39951 TOIG of: aaa39951 check: 7384 from: 1 to: 242

Initial Score = 18 Optimized Score = 107 Significance = -0.71
Residue Identity = 10% Matches = 34 Mismatches = 188
Gaps = 88 Conservative Substitutions = 20

TFIQLILISLPREYVINEACPGAEWNINMCBCEYDQIECVCPGRREVGYTTPCCRNENECDCLHP
X MGLAECCARCLVGAFFASLVAT
X 10 20

90 100 110 120 130 140 150
GCTTFEACKGCRNGSMGTLDDFYVKGFCACRAGWYGDCMRCGQVLRAPKQIILLESYPLNAHCEWTH
GLCFEYVALPFCGCGHEALYTERKLIETYPFSKNYDYEYLVNHAFOYVIYGTASFFFLYGAL-----
30 40 50 60 70 80

160 170 180 190 200 210 220
AKRGFVQLAFWMLSEFDVWCQDYVEVRDGNRDQIIRKVCGERPAPISIGSLHYLFHSDGSKNPD
-----LAEGETTGAVRQIFGDYKTTTCGKLSATFVGITYALTIVWLLVFACSAV
90 100 110 120 130

230 240 250 260 270 280 290
GFHAIVYEITACSSPCFHDGTCVLDKAGSYKACACLAGYTGRCENLLEERNCSDPGSPVNGYQKITGSPGL
PVIYFNTWTTCOSI-----
140 150

300 310 320 330 340 350 360 370
INGRHAKIGTVVSPFCNNSTYVLSGNEKRTCCQNGEWSGKPIKACBEPKISDLVRRRVLPWQVQSRETPL
--APPSTASISGLCADARNYGVLPWNAFPKVCSSYLSICTAEFQMTFHLFIAPVGAATVLSLTF
160 170 180 190 200 210 220

380 390 400 410 420 430 440
HQLYSAFSPKQKLSAPTKKRALPFGDLPMGYQHLMHQLQVEYCISPFYRRLGSSRRCTCLRTGKWSGRAPS
MIATYAFVAVKLMRGITK
230 240 X

RESULT 6
US-09-537-654-3
; Sequence 3, Application: US/09537654
; Patent No. 6,720,478
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Shi, Jintu

Db 1191 GCCAGTCGGATCTCAGACCTTCCTCCAGAGTCCACATCACTGCTGCTGGAAAT 1250
Qy 603 ValLeuAlaAspValaLagSerProGlyPheIyAsnAspThrLeuArgSerGlyValVal 622
Db 1251 GTCTGTCAGACGAGAGAGCCCTGGCTTCAAGACACACACGCTCTGGGGTGTCTC 1310
Qy 623 SerValValAspSerLeuLeuGlyGlnGlnIleGlnAspHISGlyIleProValSer 642
Db 1311 AGTGTGTGACCTGCTGCTGTGTGTGAGAGACATGAGACATGGCATCCCATGAT 1370
Qy 643 ValThrAspAsnMetPheCyAsIAserTIPgluProThrAlaProSerAspIleCyThr 662
Db 1371 GTGACTGATACATGTTCTGTGCGCAGCTGGGACCACTGCCCCCTTGTGATATCTGACT 1430
Qy 663 AlagIuThrGlyGlyIleAlaValaLagSerProGlyValaGalaSerProGluProArg 682
Db 1431 GCAGAGACAGAGGACATCGCGCTGTGTCTCCCGGAGCAGAGCATCTCCGAGCAGCG 1490
Qy 683 ThrHisLeuMetGlyLeuValaSerTIPserTyrAspIyThrCySerHisArgLeuSer 702
Db 1491 TGGCATCTGATGGAGCTGGTCAAGCTATGATATTAACATGACGACGAGCTCTCC 1550
Qy 703 ThrAlaPheThrIyValaLeuProPheIyAspTIPgluIleGlyArgAsnMetIyS 720
Db 1551 ACTGCTTCAACCAAGTGTCTCTTTTAAAGCATGAGATTGAAGAATATGAAA 1604

RESULT 5
US-09-280-116-179
Sequence 179, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280.116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: asctcin/m 12a metalloproteases
US-09-280-116-179

Alignment Scores:
Pred. No.: 5.5e-81 Length: 505
Score: 893.00 Matches: 166
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 22.64% Indels: 2
Gaps: 0

US-10-063-692-38 (1-720) x US-09-280-116-179 (1-505)

Qy 103 LeuAspAspPheTyrValIyGlyPheTyrCyAsIagIuCyArgAlaGlyTIPtyrGly 122
Db 3 TTGATGACTTCTAATGAGGGGTTTACTGTGAGAGTGGCGAGCGAGC-TGGTACGGA 61
Qy 123 GLyAspCyMetArgCyGlyGlnValaLeuArgAlaProIyGlyGlnIleLeuLeuGlu 142
Db 62 GAGAGCTGATGCGAGTGTGCGAGGTTCTGCGAGGCCCAAGGGTCAATTTTGTGGA 121
Qy 143 SerTyrProLeuAsnAlaHisCyAsIuTIPThrIleHisAlaIyAspProGlyPheValIle 162
Db 122 AGCTATCCCTTAATGCTCACTGTGAATGACCATTCATGCTTAACCTGGGTTTCTCATC 181
Qy 163 GlnLeuArgPheValaMetLeuSerLeuGlnPheAspTyrMetCyGlnTyrAspTyrVal 182
Db 182 CAACCTAAGATTGTGATGTTGAGCTGAGGTTGACTACATGTCAGATATGACTATGTT 241
183 GluValaArgAspGlyAspAsnArgAspGlyGlnIleIleIyAsArgValCyGlyAsnGlu 202

Db 242 GAGGTCGTATGAGAGCAACCGCATGCGCAGATCATCAAGCGTGTCTGTGCAACGAG 301
Qy 203 ArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSerArgGly 222
Db 302 CGGCAGCTCTCTTCAAGAGCATAGATCTCACTCACTCACTCTTCCATCTCGAATGGC 361
Qy 223 SerIyAsnAspAspGlyPheHisAlaIleTyrGlnGlnIleThrAlaCySerSerSer 242
Db 362 TCCAGAAATTTTACCGTTTCCATGCTCATTTATGAGAGATCAAGATGCTCTTATCC 421
Qy 243 ProCyAspHisAspGlyThrCyValaLeuAspIyAlaGlySerTyr-LysCyAsIaCy 262
Db 422 CTTGTTTTCATACGAGCAGCTGCTGCTTGAACAAGGCTGATCTTAACAAGTGTGCTG 481
Qy 262 GluAlaGlyTyrThrGlyGln 269
Db 482 CTTGCGAGCTATATCGGCGAG 503

RESULT 6
US-08-296-014A-3
Sequence 3, Application US/08296014A
Patent No. 5716834
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296.014A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Carcinoscopus rotundicauda
FEATURE:
NAME/KEY: CDS
LOCATION: 18...3074
US-08-296-014A-3

Alignment Scores:
Pred. No.: 1.58e-56 Length: 3448
Score: 665.00 Matches: 222